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RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/800,198

TIME: 15:42:22

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3 <110> APPLICANT: Vernet, Cornie AM
4     Fernandes, Elma
5     Shimkets, Richard A
6     Herrmann, John L
7     Majumder, Kumud
8     Mishra, Vishna
9     Mezes, Peter S
10    Rastelli, Luca
12 <120> TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
14 <130> FILE REFERENCE: 15966-697
16 <140> CURRENT APPLICATION NUMBER: 09/800198
17 <141> CURRENT FILING DATE: 2001-03-05
19 <150> PRIOR APPLICATION NUMBER: 60/186,596
20 <151> PRIOR FILING DATE: 2000-03-03
22 <160> NUMBER OF SEQ ID NOS: 98
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 771
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
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33 <222> LOCATION: (438)..(752)
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40 attggcagcc ttagaactag tgggaaggcg ggtgcgcgaa gtcgaggggc ggagagaggg 180
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46 ctttcggact cgaatcacgg ctgctgcgaa gggctagt tccggacacta gggccccaga 360
48 tcgtgtcaca tccatatgac acttggaaatg tgacagggca ggaatgtgatc tttggctgtg 420
50 aagtgtttgc ctacccc atg gcc tcc atc gag tgg agg aag gat ggc ttg 470
51      Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu
52      1          5          10
54 gac atc cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg 518
55 Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg
56      15          20          25
58 ggt gga ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct 566
59 Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala
60      30          35          40
62 gtg cgt ccc agt gat gag ggc act tac cgc tgc ctt gcc cgc aat gcc 614
63 Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Ala Arg Asn Ala
64      45          50          55
66 ctg ggt caa gtg gag gcc cct gct agc ttg aca gtg ctc aca cct gac 662
67 Leu Gly Gln Val Glu Ala Pro Ala Ser Leu Thr Val Leu Thr Pro Asp
68 60          65          70          75
70 cag ctg aac tct aca ggc atc ccc cag ctg cga tca cta aac ctg gtt 710

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71 Gln Leu Asn Ser Thr Gly Ile Pro Gln Leu Arg Ser Leu Asn Leu Val
72                80                85                90
74 cct gag gag gag gct gag agt gaa gag aat gac gat tac tac      752
75 Pro Glu Glu Glu Ala Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
76                95                100                105
78 taggtccaga gctctggcc      771
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83 <212> TYPE: PRT
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90 Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly Pro Gln Arg
91          20          25          30
93 Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg Pro Ser Asp
94          35          40          45
96 Glu Gly Thr Tyr Arg Cys Leu Ala Arg Asn Ala Leu Gly Gln Val Glu
97          50          55          60
99 Ala Pro Ala Ser Leu Thr Val Leu Thr Pro Asp Gln Leu Asn Ser Thr
100 65          70          75          80
102 Gly Ile Pro Gln Leu Arg Ser Leu Asn Leu Val Pro Glu Glu Glu Ala
103          85          90          95
105 Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
106          100          105
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124 gcccgggcag gtcattaatt ccatttcttt ttagagtatc acagctttct ctttactga 180
126 ccaccctttg cttcctgtca gaaagccctg gacagaactc tctgtgggat tctgcccatg 240
128 tttctgagat atcgccctca ttgtcctggc tgggctgtcg ggtctgcccg ttttacagat 300
130 gggcaaactg gagtggaag tatccgggtg gcttcctcag gcctgcagct ggtggagcag 360
132 ctactgaaac aatcaggagc ccagaagctt tgaagtcaca agaagagaag actcccaga 419
134 atg cag tgt gat gtt ggt gat gga cgc ctg ttt cgc ctt tca ctt aaa 467
135 Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys
136 1          5          10          15
138 cgt gcc ctt tcc agc tgc cct gac ctc ttt ggg ctt tcc agc cgc aac 515
139 Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn
140          20          25          30
142 gag ctg ctg gcc tcc tgc ggg aag aag ttc tgc agc cga ggg agc cgg 563
143 Glu Leu Leu Ala Ser Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg
144          35          40          45

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147	Cys	Val	Leu	Ser	Arg	Lys	Thr	Gly	Glu	Pro	Glu	Cys	Gln	Cys	Leu	Glu	
148	50						55				60						
150	gca	tgc	agg	ccc	agc	tac	gtg	cct	gtg	tgc	ggc	tct	gat	ggg	agg	ttt	659
151	Ala	Cys	Arg	Pro	Ser	Tyr	Val	Pro	Val	Cys	Gly	Ser	Asp	Gly	Arg	Phe	
152	65					70				75						80	
154	tat	gaa	aac	cac	tgt	aag	ctc	cac	cgt	gct	gct	tgc	ctc	ctg	gga	aag	707
155	Tyr	Glu	Asn	His	Cys	Lys	Leu	His	Arg	Ala	Ala	Cys	Leu	Leu	Gly	Lys	
156				85					90					95			
158	agg	atc	acc	gtc	atc	cac	agc	aag	gac	tgt	ttc	ctc	aaa	ggt	gac	acg	755
159	Arg	Ile	Thr	Val	Ile	His	Ser	Lys	Asp	Cys	Phe	Leu	Lys	Gly	Asp	Thr	
160				100					105					110			
162	tgc	acc	atg	gcc	ggc	tac	gcc	cgc	ttg	aag	aat	gtc	ctt	ctg	gca	ctc	803
163	Cys	Thr	Met	Ala	Gly	Tyr	Ala	Arg	Leu	Lys	Asn	Val	Leu	Leu	Ala	Leu	
164			115				120					125					
166	cag	acc	cgt	ctg	cag	cca	ctc	caa	gaa	gga	gac	agc	aga	caa	gac	cct	851
167	Gln	Thr	Arg	Leu	Gln	Pro	Leu	Gln	Glu	Gly	Asp	Ser	Arg	Gln	Asp	Pro	
168			130				135					140					
170	gcc	tcc	cag	aag	cgc	ctc	ctg	gtg	gaa	tct	ctg	ttc	agg	gac	tta	gat	899
171	Ala	Ser	Gln	Lys	Arg	Leu	Leu	Val	Glu	Ser	Leu	Phe	Arg	Asp	Leu	Asp	
172	145					150					155					160	
174	gca	gat	ggc	aat	ggc	cac	ctc	agc	agc	tcc	gaa	ctg	gct	cag	cat	gtg	947
175	Ala	Asp	Gly	Asn	Gly	His	Leu	Ser	Ser	Ser	Glu	Leu	Ala	Gln	His	Val	
176				165						170					175		
178	ctg	aag	aag	cag	gac	ctg	gat	gaa	gac	tta	ctt	ggt	tgc	tca	cca	ggt	995
179	Leu	Lys	Lys	Gln	Asp	Leu	Asp	Glu	Asp	Leu	Leu	Gly	Cys	Ser	Pro	Gly	
180				180					185					190			
182	gac	ctc	ctc	cga	ttt	gac	gat	tac	aac	agt	gac	agc	tcc	ctg	acc	ctc	1043
183	Asp	Leu	Leu	Arg	Phe	Asp	Asp	Tyr	Asn	Ser	Asp	Ser	Ser	Leu	Thr	Leu	
184			195					200					205				
186	cgc	gag	ttc	tac	atg	gcc	ttc	caa	gtg	gtt	cag	ctc	agc	ctc	gcc	ccc	1091
187	Arg	Glu	Phe	Tyr	Met	Ala	Phe	Gln	Val	Val	Gln	Leu	Ser	Leu	Ala	Pro	
188		210				215					220						
190	gag	gac	agg	gtc	agt	gtg	acc	aca	gtg	acc	gtg	ggg	ctg	agc	aca	gtg	1139
191	Glu	Asp	Arg	Val	Ser	Val	Thr	Thr	Val	Thr	Val	Gly	Leu	Ser	Thr	Val	
192	225					230					235					240	
194	ctg	acc	tgc	gcc	gtc	cat	gga	gac	ctg	agg	cca	cca	atc	atc	tgg	aag	1187
195	Leu	Thr	Cys	Ala	Val	His	Gly	Asp	Leu	Arg	Pro	Pro	Ile	Ile	Trp	Lys	
196				245					250						255		
198	cgc	aac	ggg	ctc	acc	ctg	aac	ttc	ctg	gac	ttg	gaa	gac	atc	aat	gac	1235
199	Arg	Asn	Gly	Leu	Thr	Leu	Asn	Phe	Leu	Asp	Leu	Glu	Asp	Ile	Asn	Asp	
200				260					265					270			
202	ttt	gga	gag	gat	gat	tcc	ctg	tac	atc	acc	aag	gtg	acc	acc	atc	cac	1283
203	Phe	Gly	Glu	Asp	Asp	Ser	Leu	Tyr	Ile	Thr	Lys	Val	Thr	Thr	Ile	His	
204			275					280					285				
206	atg	ggc	aat	tac	acc	tgc	cat	gct	tcc	ggc	cac	gag	cag	ctg	ttc	cag	1331
207	Met	Gly	Asn	Tyr	Thr	Cys	His	Ala	Ser	Gly	His	Glu	Gln	Leu	Phe	Gln	
208		290				295					300						
210	acc	cac	gtc	ctg	cag	gtg	aat	gtg	ccg	cca	gtc	atc	cgt	gtc	tat	cca	1379

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214	gag	agc	cag	gca	cag	gag	cct	gga	gtg	gca	gcc	agc	cta	aga	tgc	cat	1427
215	Glu	Ser	Gln	Ala	Gln	Glu	Pro	Gly	Val	Ala	Ala	Ser	Leu	Arg	Cys	His	
216					325					330					335		
218	gct	gag	ggc	att	ccc	atg	ccc	aga	atc	act	tgg	ctg	aaa	aac	ggc	gtg	1475
219	Ala	Glu	Gly	Ile	Pro	Met	Pro	Arg	Ile	Thr	Trp	Leu	Lys	Asn	Gly	Val	
220				340					345					350			
222	gat	gtc	tca	act	cag	atg	tcc	aaa	cag	ctc	tcc	ctt	tta	gcc	aat	ggg	1523
223	Asp	Val	Ser	Thr	Gln	Met	Ser	Lys	Gln	Leu	Ser	Leu	Leu	Ala	Asn	Gly	
224			355					360					365				
226	agc	gaa	ctc	cac	atc	agc	agt	gtt	cgg	tat	gaa	gac	aca	ggg	gca	tac	1571
227	Ser	Glu	Leu	His	Ile	Ser	Ser	Val	Arg	Tyr	Glu	Asp	Thr	Gly	Ala	Tyr	
228	370					375					380						
230	acc	tgc	att	gcc	aaa	aat	gaa	gtg	ggt	gtg	gat	gaa	gat	atc	tcc	tgc	1619
231	Thr	Cys	Ile	Ala	Lys	Asn	Glu	Val	Gly	Val	Asp	Glu	Asp	Ile	Ser	Ser	
232	385				390					395						400	
234	ctc	ttc	att	gaa	gac	tca	gct	aga	aag	acc	ctt	gca	aac	atc	ctg	tgg	1667
235	Leu	Phe	Ile	Glu	Asp	Ser	Ala	Arg	Lys	Thr	Leu	Ala	Asn	Ile	Leu	Trp	
236				405					410						415		
238	cga	gag	gaa	ggc	ctc	agc	gtg	gga	aac	atg	ttc	tat	gtc	ttc	tcc	gac	1715
239	Arg	Glu	Glu	Gly	Leu	Ser	Val	Gly	Asn	Met	Phe	Tyr	Val	Phe	Ser	Asp	
240				420				425					430				
242	gac	ggt	atc	atc	gtc	atc	cat	cct	gtg	gac	tgt	gag	atc	cag	agg	cac	1763
243	Asp	Gly	Ile	Ile	Val	Ile	His	Pro	Val	Asp	Cys	Glu	Ile	Gln	Arg	His	
244			435				440					445					
246	ctc	aaa	ccc	acg	gaa	aag	att	ttc	atg	agc	tat	gaa	gaa	atc	tgt	cct	1811
247	Leu	Lys	Pro	Thr	Glu	Lys	Ile	Phe	Met	Ser	Tyr	Glu	Glu	Ile	Cys	Pro	
248	450					455					460						
250	caa	aga	gaa	aaa	aat	gca	acc	cag	ccc	tgc	cag	tgg	gta	tct	gca	gtc	1859
251	Gln	Arg	Glu	Lys	Asn	Ala	Thr	Gln	Pro	Cys	Gln	Trp	Val	Ser	Ala	Val	
252	465				470					475					480		
254	aat	gtc	cgg	aac	cgg	tac	atc	tat	gtg	gcc	cag	cca	gca	ctg	agc	aga	1907
255	Asn	Val	Arg	Asn	Arg	Tyr	Ile	Tyr	Val	Ala	Gln	Pro	Ala	Leu	Ser	Arg	
256				485				490						495			
258	gtc	ctt	gtg	gtc	gac	atc	caa	gcc	cag	aaa	gtc	cta	cag	tcc	ata	ggt	1955
259	Val	Leu	Val	Val	Asp	Ile	Gln	Ala	Gln	Lys	Val	Leu	Gln	Ser	Ile	Gly	
260				500				505						510			
262	gtg	gac	cct	ctg	ccg	gct	aag	ctg	tcc	tat	gac	aag	tca	cat	gac	caa	2003
263	Val	Asp	Pro	Leu	Pro	Ala	Lys	Leu	Ser	Tyr	Asp	Lys	Ser	His	Asp	Gln	
264			515				520						525				
266	gtg	tgg	gtc	ctg	agc	tgg	ggg	gac	gtg	cac	aag	tcc	cga	cca	agt	ctc	2051
267	Val	Trp	Val	Leu	Ser	Trp	Gly	Asp	Val	His	Lys	Ser	Arg	Pro	Ser	Leu	
268	530					535					540						
270	cag	gtg	atc	aca	gaa	gcc	agc	acc	ggc	cag	agc	cag	cac	ctc	atc	cgc	2099
271	Gln	Val	Ile	Thr	Glu	Ala	Ser	Thr	Gly	Gln	Ser	Gln	His	Leu	Ile	Arg	
272	545					550					555					560	
274	aca	ccc	ttt	gca	gga	gtg	gat	gat	ttc	ttc	att	ccc	cca	aca	aac	ctc	2147
275	Thr	Pro	Phe	Ala	Gly	Val	Asp	Asp	Phe	Phe	Ile	Pro	Pro	Thr	Asn	Leu	

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279	Ile Ile Asn His Ile Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro						
280		580		585		590	
282	gca gtc cac aag gtg gac ctg gaa aca atg atg ccc ctc aag acc atc	2243					
283	Ala Val His Lys Val Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile						
284		595		600		605	
286	ggc ctg cac cac cat ggc tgc gtg ccc cag gcc atg gca cac acc cac	2291					
287	Gly Leu His His His Gly Cys Val Pro Gln Ala Met Ala His Thr His						
288		610		615		620	
290	ctg ggc ggc tac ttc ttc atc cag tgc cga cag gac agc ccc gcc tct	2339					
291	Leu Gly Gly Tyr Phe Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser						
292	625		630		635		640
294	gct gcc cga cag ctg ctc gtt gac agt gtc aca gac tct gtg ctt ggc	2387					
295	Ala Ala Arg Gln Leu Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly						
296		645		650		655	
298	ccc aat ggt gat gta aca ggc acc cca cac aca tcc ccc gac ggg cgc	2435					
299	Pro Asn Gly Asp Val Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg						
300		660		665		670	
302	ttc ata gtc agt gct gca gct gac agc ccc tgg ctg cac gtg cag gag	2483					
303	Phe Ile Val Ser Ala Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu						
304		675		680		685	
306	atc aca gtg cgg ggc gag atc cag acc ctg tat gac ctg caa ata aac	2531					
307	Ile Thr Val Arg Gly Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn						
308		690		695		700	
310	tcg ggc atc tca gac ttg gcc ttc cag cgc tcc ttc act gaa agc aat	2579					
311	Ser Gly Ile Ser Asp Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn						
312	705		710		715		720
314	caa tac aac atc tac gcg gct ctg cac acg gag ccg gac ctg ctg ttc	2627					
315	Gln Tyr Asn Ile Tyr Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe						
316		725		730		735	
318	ctg gag ctg tcc acg ggg aag gtg ggc atg ctg aag aac tta aag gag	2675					
319	Leu Glu Leu Ser Thr Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu						
320		740		745		750	
322	cca ccc gca ggg cca gct cag ccc tgg ggg ggt acc cac aga atc atg	2723					
323	Pro Pro Ala Gly Pro Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met						
324		755		760		765	
326	agg gac agt ggg ctg ttt gga cag tac ctc ctc aca cca gcc cga gag	2771					
327	Arg Asp Ser Gly Leu Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu						
328		770		775		780	
330	tca ctg ttc ctc atc aat ggg aga caa aac acg ctg cgg tgt gag gtg	2819					
331	Ser Leu Phe Leu Ile Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val						
332	785		790		795		800
334	tca ggt ata aag ggg ggg acc aca gtg gtg tgg gtg ggt gag gta	2864					
335	Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val						
336		805		810		815	
338	tgaagggccc agagcagagc cctggggccaa ggaacacccc ctagtcctga cactgcagcc	2924					
340	tcaagcaggt acgctgtaca tttttacaga caaaagcaaa aacctgtact cgctttgtgg	2984					
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